PAGE: 1

**RAW SEQUENCE LISTING**
**PATENT APPLICATION** *US/09/236,468*

DATE: 02/10/1999
TIME: 16:12:12

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*INPUT SET: S30588.raw*

> This Raw Listing contains the General
> Information Section and up to the first 5 pages.

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 1                                    SEQUENCE LISTING       ENTERED
 2
 3   (1)     General Information:
 4
 5       (i) APPLICANT: Soppet, Daniel R
 6                      Yi, Li
 7                      Rosen, Craig A
 8                      Ruben, Steven
 9
10      (ii) TITLE OF INVENTION: G-Protein Parathyroid Hormone receptor
11            HLTDG74
12
13     (iii) NUMBER OF SEQUENCES: 8
14
15      (iv) CORRESPONDENCE ADDRESS:
16            (A) ADDRESSEE: Human Genome Sciences, Inc.
17            (B) STREET: 9410 Key West Ave
18            (C) CITY: Rockville
19            (D) STATE: MD
20            (E) COUNTRY: USA
21            (F) ZIP: 20850
22
23       (v) COMPUTER READABLE FORM:
24            (A) MEDIUM TYPE: Floppy disk
25            (B) COMPUTER: IBM PC compatible
26            (C) OPERATING SYSTEM: PC-DOS/MS-DOS
27            (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
28
29      (vi) CURRENT APPLICATION DATA:
30            (A) APPLICATION NUMBER:
31            (B) FILING DATE:
32            (C) CLASSIFICATION:
33
34     (vi) PRIOR APPLICATION DATA:
35            (A) APPLICATION NUMBER:  08/468,011
36            (B) FILING DATE: 06-JUN-1995
37            (C) CLASSIFICATION:
38
39    (viii) ATTORNEY/AGENT INFORMATION:
40            (A) NAME: A. Anders Brookes
41            (B) REGISTRATION NUMBER: 36,373
42            (C) REFERENCE/DOCKET NUMBER: PF201D1
43
44      (ix) TELECOMMUNICATION INFORMATION:
45            (A) TELEPHONE: 201-994-1700
46            (B) TELEFAX: 201-994-1744
```

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47
48
49     (2) INFORMATION FOR SEQ ID NO:1:
50
51         (i) SEQUENCE CHARACTERISTICS:
52             (A) LENGTH: 2003 base pairs
53             (B) TYPE: nucleic acid
54             (C) STRANDEDNESS: single
55             (D) TOPOLOGY: linear
56
57         (ii) MOLECULE TYPE: cDNA
58
59
60         (ix) FEATURE:
61             (A) NAME/KEY: CDS
62             (B) LOCATION: 90..1712
63
64
65         (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:
66
67  GTTTGCTCTG GGCAGCCAAG TTGGCATATT GGAAGCTTTT TCCGGGCTCT GGAGGAGGGT          60
68
69  CCCTGCTTCT TCCTACAGCC GTTCCGGGC ATG GCC TGG CTG GGG GCG TCG CTC          113
70                                    Met Ala Trp Leu Gly Ala Ser Leu
71                                     1               5
72
73  CAC GTC TGG GGT TGG CTA ATG CTC GGC AGC TGC CTC CTG GCC AGA GCC          161
74  His Val Trp Gly Trp Leu Met Leu Gly Ser Cys Leu Leu Ala Arg Ala
75      10              15                  20
76
77  CAG CTG GAT TCT GAT GGC ACC ATC ACT ATA GAG GAG CAG ATT GTC CTT          209
78  Gln Leu Asp Ser Asp Gly Thr Ile Thr Ile Glu Glu Gln Ile Val Leu
79  25              30                  35                      40
80
81  GTG CTG AAA GCG AAA GTA CAA TGT GAA CTC AAC ATC ACA GCT CAA CTC          257
82  Val Leu Lys Ala Lys Val Gln Cys Glu Leu Asn Ile Thr Ala Gln Leu
83              45                  50                  55
84
85  CAG GAG GGA GAA GGT AAT TGT TTC CCT GAA TGG GAT GGA CTC ATT TGT          305
86  Gln Glu Gly Glu Gly Asn Cys Phe Pro Glu Trp Asp Gly Leu Ile Cys
87              60                  65                  70
88
89  TGG CCC AGA GGA ACA GTG GGG AAA ATA TCG GCT GTT CCA TGC CCT CCT          353
90  Trp Pro Arg Gly Thr Val Gly Lys Ile Ser Ala Val Pro Cys Pro Pro
91          75                  80                  85
92
93  TAT ATT TAT GAC TTC AAC CAT AAA GGA GTT GCT TTC CGA CAC TGT AAC          401
94  Tyr Ile Tyr Asp Phe Asn His Lys Gly Val Ala Phe Arg His Cys Asn
95          90                  95                  100
96
97  CCC AAT GGA ACA TGG GAT TTT ATG CAC AGC TTA AAT AAA ACA TGG GCC          449
98  Pro Asn Gly Thr Trp Asp Phe Met His Ser Leu Asn Lys Thr Trp Ala
99  105                 110                 115                 120
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101   AAT TAT TCA GAC TGC CTT CGC TTT CTG CAG CCA GAT ATC AGC ATA GGA        497
102   Asn Tyr Ser Asp Cys Leu Arg Phe Leu Gln Pro Asp Ile Ser Ile Gly
103                   125                 130                 135
104
105   AAG CAA GAA TTC TGT GAA CGC CTC TAT GTA ATG TAT ACC GTT GGC TAC        545
106   Lys Gln Glu Phe Cys Glu Arg Leu Tyr Val Met Tyr Thr Val Gly Tyr
107                   140                 145                 150
108
109   TCC ATC TCT TTT GGT TCC TTG GCT GTG GCT ATT CTC ATC ATT GGT TAC        593
110   Ser Ile Ser Phe Gly Ser Leu Ala Val Ala Ile Leu Ile Ile Gly Tyr
111                   155                 160                 165
112
113   TTC AGA CGA TTG CAT TGC ACT AGG AAC TAT ATC CAC ATG CAC TTA TTT        641
114   Phe Arg Arg Leu His Cys Thr Arg Asn Tyr Ile His Met His Leu Phe
115       170                 175                 180
116
117   GTG TCT TTC ATG CTG AGA GCT ACA AGC ATC TTT GTC AAA GAC AGA GTA        689
118   Val Ser Phe Met Leu Arg Ala Thr Ser Ile Phe Val Lys Asp Arg Val
119   185                 190                 195                 200
120
121   GTC CAT GCT CAC ATA GGA GTA AAG GAG CTG GAG TCC CTA ATA ATG CAG        737
122   Val His Ala His Ile Gly Val Lys Glu Leu Glu Ser Leu Ile Met Gln
123                   205                 210                 215
124
125   GAT GAC CCA CAA AAT TCC ATT GAG GCA ACT TCT GTG GAC AAA TCA CAA        785
126   Asp Asp Pro Gln Asn Ser Ile Glu Ala Thr Ser Val Asp Lys Ser Gln
127                   220                 225                 230
128
129   TAT ATC GGG TGC AAG ATT GCT GTT GTG ATG TTT ATT TAC TTC CTG GCT        833
130   Tyr Ile Gly Cys Lys Ile Ala Val Val Met Phe Ile Tyr Phe Leu Ala
131                   235                 240                 245
132
133   ACA AAT TAT TAT TGG ATC CTG GTG GAA GGT CTC TAC CTG CAT AAT CTC        881
134   Thr Asn Tyr Tyr Trp Ile Leu Val Glu Gly Leu Tyr Leu His Asn Leu
135       250                 255                 260
136
137   ATC TTT GTG GCT TTC TTT TCG GAC ACC AAA TAC CTG TGG GGC TTC ATC        929
138   Ile Phe Val Ala Phe Phe Ser Asp Thr Lys Tyr Leu Trp Gly Phe Ile
139   265                 270                 275                 280
140
141   TTG ATA GGC TGG GGG TTT CCA GCA GCA TTT GTT GCA GCA TGG GCT GTG        977
142   Leu Ile Gly Trp Gly Phe Pro Ala Ala Phe Val Ala Ala Trp Ala Val
143                   285                 290                 295
144
145   GCA CGA GCA ACT CTG GCT GAT GCG AGG TGC TGG GAA CTT AGT GCT GGA        1025
146   Ala Arg Ala Thr Leu Ala Asp Ala Arg Cys Trp Glu Leu Ser Ala Gly
147                   300                 305                 310
148
149   GAC ATC AAG TGG ATT TAT CAA GCA CCG ATC TTA GCA GCT ATT GGG CTG        1073
150   Asp Ile Lys Trp Ile Tyr Gln Ala Pro Ile Leu Ala Ala Ile Gly Leu
151                   315                 320                 325
152
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153    AAT TTT ATT CTG TTT CTG AAT ACG GTT AGA GTT CTA GCT ACC AAA ATC        1121
154    Asn Phe Ile Leu Phe Leu Asn Thr Val Arg Val Leu Ala Thr Lys Ile
155        330             335             340
156
157    TGG GAG ACC AAT GCA GTT GGG CAT GAC ACA AGG AAG CAA TAC AGG AAA        1169
158    Trp Glu Thr Asn Ala Val Gly His Asp Thr Arg Lys Gln Tyr Arg Lys
159    345             350             355             360
160
161    CTG GCC AAA TCG ACA CTG GTC CTG GTC CTA GTC TTT GGA GTG CAT TAC        1217
162    Leu Ala Lys Ser Thr Leu Val Leu Val Leu Val Phe Gly Val His Tyr
163            365             370             375
164
165    ATC GTG TTC GTG TGC CTG CCT CAC TCC TTC ACT GGG CTC GGG TGG GAG        1265
166    Ile Val Phe Val Cys Leu Pro His Ser Phe Thr Gly Leu Gly Trp Glu
167            380             385             390
168
169    ATC CGC ATG CAC TGT GAG CTC TTC TTC AAC TCC TTT CAG GGT TTC TTT        1313
170    Ile Arg Met His Cys Glu Leu Phe Phe Asn Ser Phe Gln Gly Phe Phe
171            395             400             405
172
173    GTG TCT ATC ATC TAC TGC TAC TGC AAT GGA GAG GTT CAG GCA GAG GTG        1361
174    Val Ser Ile Ile Tyr Cys Tyr Cys Asn Gly Glu Val Gln Ala Glu Val
175        410             415             420
176
177    AAG AAG ATG TGG AGT CGG TGG AAT CTC TCC GTG GAC TGG AAA AGG ACA        1409
178    Lys Lys Met Trp Ser Arg Trp Asn Leu Ser Val Asp Trp Lys Arg Thr
179    425             430             435             440
180
181    CCG CCA TGT GGC AGC CGC AGA TGC GGC TCA GTG CTC ACC ACC GTG ACG        1457
182    Pro Pro Cys Gly Ser Arg Arg Cys Gly Ser Val Leu Thr Thr Val Thr
183            445             450             455
184
185    CAC AGC ACC AGC AGC CAG TCA CAG GTG GCG GCA GCA CAC GCA TGG TGC        1505
186    His Ser Thr Ser Ser Gln Ser Gln Val Ala Ala Ala His Ala Trp Cys
187            460             465             470
188
189    TTA TCT CTG GCA AAG CTG CCA AGA TCG CCA GCA GAC AGC CTG ACA GCC        1553
190    Leu Ser Leu Ala Lys Leu Pro Arg Ser Pro Ala Asp Ser Leu Thr Ala
191            475             480             485
192
193    ACA TCA CTT TAC CTG GCT ATG TCT GGA GTA ACT CAG AGC AGG ACT GCC        1601
194    Thr Ser Leu Tyr Leu Ala Met Ser Gly Val Thr Gln Ser Arg Thr Ala
195        490             495             500
196
197    TCA CAC ACT CTC TCC ACG AGG AGC AAC AAG GAA GAT AGT GGG AGG CAG        1649
198    Ser His Thr Leu Ser Thr Arg Ser Asn Lys Glu Asp Ser Gly Arg Gln
199    505             510             515             520
200
201    AGA GAT GAT ATT CTA ATG GAG AAG CCT TCC AGG CCT ATG GAA TCT AAC        1697
202    Arg Asp Asp Ile Leu Met Glu Lys Pro Ser Arg Pro Met Glu Ser Asn
203            525             530             535
204
205    CCA GAC ACT GAA GGA TGACAAGGAG AAACTGAGGA TGTTCTCTGA ATGGACATGT       1752
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206   Pro Asp Thr Glu Gly
207               540
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209   GTGGCTGACT TTCATGGGCT GGTCCAATGG CTGGTTGTGT GAGAGGGCTT GGCTGATACT   1812
210
211   CCTATGCTTG AGCACAAAGG CTGAAAATTC AGTTAAGGTG TTACTTAATA ATAGTTTTTA   1872
212
213   GGCTCCATGA ATTGGCTCCT GTAAATACTA ACGACATGAA AATGCAAGTG TCAATGGAGT   1932
214
215   AGTTTATTAC CTTCTATTGG CATCAAGTTT TCCTCTAAAT TAATGTATGG TATTTGCTCT   1992
216
217   GTGATTGTTC A                                                        2003
218
219
220   (2) INFORMATION FOR SEQ ID NO:2:
221
222        (i) SEQUENCE CHARACTERISTICS:
223             (A) LENGTH: 541 amino acids
224             (B) TYPE: amino acid
225             (D) TOPOLOGY: linear
226
227        (ii) MOLECULE TYPE: protein
228
229        (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:
230
231   Met Ala Trp Leu Gly Ala Ser Leu His Val Trp Gly Trp Leu Met Leu
232    1               5              10                  15
233
234   Gly Ser Cys Leu Leu Ala Arg Ala Gln Leu Asp Ser Asp Gly Thr Ile
235             20              25              30
236
237   Thr Ile Glu Glu Gln Ile Val Leu Val Leu Lys Ala Lys Val Gln Cys
238          35              40              45
239
240   Glu Leu Asn Ile Thr Ala Gln Leu Gln Glu Gly Glu Gly Asn Cys Phe
241       50              55              60
242
243   Pro Glu Trp Asp Gly Leu Ile Cys Trp Pro Arg Gly Thr Val Gly Lys
244    65              70              75              80
245
246   Ile Ser Ala Val Pro Cys Pro Pro Tyr Ile Tyr Asp Phe Asn His Lys
247             85              90              95
248
249   Gly Val Ala Phe Arg His Cys Asn Pro Asn Gly Thr Trp Asp Phe Met
250             100             105             110
251
252   His Ser Leu Asn Lys Thr Trp Ala Asn Tyr Ser Asp Cys Leu Arg Phe
253          115             120             125
254
255   Leu Gln Pro Asp Ile Ser Ile Gly Lys Gln Glu Phe Cys Glu Arg Leu
256          130             135             140
257
258   Tyr Val Met Tyr Thr Val Gly Tyr Ser Ile Ser Phe Gly Ser Leu Ala
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**SEQUENCE VERIFICATION REPORT**
PATENT APPLICATION   *US/09/236,468*

*INPUT SET: S30588.raw*

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